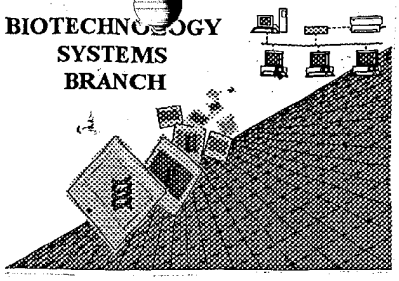
05-90
1018

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/773,307

Source: OIPE

Date Processed by STIC: 10/19/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/773,307

DATE: 10/19/2001
TIME: 14:05:54

Input Set : A:\pbm37seq.txt
Output Set: N:\CRF3\10192001\I773307.raw

Does Not Comply
Corrected Diskette Needed
pp 1-3

```
     4 <110> APPLICANT: BML, INC.
     6 <120> TITLE OF INVENTION: Method of Detecting Risk Factor for Onset of Diabetes
     8 <130> FILE REFERENCE: PBM37
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/773,307
C--> 11 <141> CURRENT FILING DATE: 2001-01-31
E--> 13 <160> NUMBER OF SEQ ID NOS: 23  22 shown (p3)
    15 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
    17 <210> SEQ ID NO: 1
    18 <211> LENGTH: 1305  1411
    19 <212> TYPE: DNA
    20 <213> ORGANISM: Hominidae
    22 <220> FEATURE:
    23 <221> NAME/KEY: CDS
    24 <222> LOCATION: (1)..(900)
    26 <400> SEQUENCE: 1
E--> 28        delete -103 aaa cagaagggga ggtgcagttt cagaacccag ccagcctctc -61  43
E--> 30 tcttgctgcc tagcctcctg ccggcctcat cttcgcccag ccaaccccgc ctggagccct -1  103
E--> 33 atg gcc aac tgc gag ttc agc ccg gtg tcc ggg gac aaa ccc tgc tgc  48
    34 Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys
    35   1               5                  10                  15
E--> 37 cgg ctc tct agg aga gcc caa ctc tgt ctt ggc gtc agt atc ctg gtc  96
    38 Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val
    39               20                  25                  30
E--> 41 ctg atc ctc gtc gtg gtg ctc gcg gtg gtc gtc ccg agg tgg cgc cag  144
    42 Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
    43           35                  40                  45
E--> 45 cag tgg agc ggt ccg ggc acc acc aag cgc ttt ccc gag acc gtc ctg  192
    46 Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu
    47       50                  55                  60
E--> 49 gcg cga tgc gtc aag tac act gaa att cat cct gag atg aga cat gta  240
    50 Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val
    51   65                  70                  75                  80
E--> 53 gac tgc caa agt gta tgg gat gct ttc aag ggt gca ttt att tca aaa  288
    54 Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys
    55                   85                  90                  95
E--> 57 cat cct tgc aac att act gaa gaa gac tat cag cca cta atg aag ttg  336
    58 His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu
    59               100                 105                 110
E--> 61 gga act cag acc gta cct tgc aac aag att ctt ctt tgg agc aga ata  384
    62 Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile
    63           115                 120                 125
E--> 65 aaa gat ctg gcc cat cag ttc aca cag gtc cag cgg gac atg ttc acc  432
    66 Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr
```

Per 1.822(c)(6) of Sequence Rules, "The enumeration of nucleotide bases shall start at the first base of the sequence with number 1." Invalid - do not use negative nos.

nos. off

RAW SEQUENCE LISTING DATE: 10/19/2001
PATENT APPLICATION: US/09/773,307 TIME: 14:05:54

Input Set : A:\pbm37seq.txt
Output Set: N:\CRF3\10192001\I773307.raw

```
     67     130                 135                 140
E--> 69 ctg gag gac acg ctg cta ggc tac ctt gct gat gac ctc aca tgg tgt  480
     70 Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys
     71 145                 150                 155                 160
E--> 73 ggt gaa ttc aac act tcc aaa ata aac tat caa tct tgc cca gac tgg  528
     74 Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp
     75                 165                 170                 175
E--> 77 aga aag gac tgc agc aac aac cct gtt tca gta ttc tgg aaa acg gtt  576
     78 Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val
     79             180                 185                 190
E--> 81 tcc cgc agg ttt gca gaa gct gcc tgt gat gtg gtc cat gtg atg ctc  624
     82 Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu
     83         195                 200                 205
E--> 85 aat gga tcc cgc agt aaa atc ttt gac aaa aac agc act ttt ggg agt  672
     86 Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser
     87     210                 215                 220
E--> 89 gtg gaa gtc cat aat ttg caa cca gag aag gtt cag aca cta gag gcc  720
     90 Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala
     91 225                 230                 235                 240
E--> 93 tgg gtg ata cat ggt gga aga gaa gat tcc aga gac tta tgc cag gat  768
     94 Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp
     95                 245                 250                 255
E--> 97 ccc acc ata aaa gag ctg gaa tcg att ata agc aaa agg aat att caa  816
     98 Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln
     99             260                 265                 270
E--> 101 ttt tcc tgc aag aat atc tac aga cct gac aag ttt ctt cag tgt gtg  864
     102 Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val
     103         275                 280                 285
E--> 105 aaa aat cct gag gat tca tct tgc aca tct gag atc tgagccagtc       910
     106 Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile
     107     290                 295                 300
E--> 109 gctgtggttg ttttagctcc ttgactcctt gtggtttatg tcatcataca tgactcagca 970
E--> 111 tacctgctgg tgcagagctg aagattttgg agggtcctcc acaataaggt caatgccaga 1030
E--> 113 gacggaagcc tttttcccca aagtcttaaa ataacttata tcatcagcat acctttattg 1090
E--> 115 tgatctatca atagtcaaga aaaattattg tataagatta gaatgaaaat tgtatgttaa 1150
E--> 117 gttacttcac tttaattctc atgtgatcct tttatgttat ttatatattg gtaacatcct 1210
E--> 119 ttctattgaa aaatcaccac accaaacctc tcttattaga acaggcaagt gaagaaaagt 1270
E--> 121 gaatgctcaa gtttttcaga aagcattaca tttcc                          1305
```

nos. off

<210> 22
<211> 66
<212> DNA
<213> Hominidae

last sequence in file

<400> 22
ttagcgaatt ggacgacaga tgtatcctac ggtctcttga tttccttttt tgctttcttg 60

tcatag 66

VERIFICATION SUMMARY DATE: 10/19/2001
PATENT APPLICATION: **US/09/773,307** TIME: 14:05:55

Input Set : **A:\pbm37seq.txt**
Output Set: **N:\CRF3\10192001\I773307.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:254 E: No. of Bases conflict, LENGTH:Input:-61 Counted:45 SEQ:1
L:28 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
M:254 Repeated in SeqNo=1
L:121 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1305 Found:1411 SEQ:1
L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (23) Counted (22)